REMARKS

Claims 1-44 are in this application; claims 1-6, 8-11, 13, 19-23, 37 and 40-44 have been examined. Claims 1, 6, 8, 9, 10, 19, 23 and 37 have been amended to specify a range of lengths for the peptides of the invention; support is found in the as-filed Specification, Paragraph [0172]. Claim 13 has been amended to incorporate a transitional phrase in accordance with the Examiner's request. The Specification has been amended to include sequence identifiers and a replacement Sequence Listing in compliance with 37 C.F.R. 1.821-1.825. None of the amendments made herein constitutes the addition of new matter.

The Specification

The Specification has been objected to for failing to comply with sequence rules.

In the interest of advancing prosecution and without acquiescing to the rejection, Applicants have amended the Specification to comply with 37 CFR 1.821-1.825. In addition, Applicants provide herewith a replacement Sequence Listing which adds sequence information missing in the prior Sequence Listing. New SEQ ID NOs:107-109 are supported at Paragraph [0098], page 22, and SEQ ID NO:110 and SEQ ID NO:111 are supported by as filed Fig. 17A. Accordingly, the replacement Sequence Listing does not add new matter.

The Patent Office has objected to the drawings for lack of sequence identifiers. Applicants respectfully submit that the present amendments to the Specification, specifically in the descriptions of the relevant figures (Paragraphs [0056], [0065], [0066], [0067] and [0071]-[0076] renders the objection to the drawings moot.

The Claims

Claim 13 is objected to for failure to include a transitional phrase. The Examiner has examined the claims based on an interpretation of "comprising".

In the interest of advancing prosecution and without acquiescing to the rejection, Applicants have amended claim 13 to recite "comprising" rather than "is". For clarity, Applicants note that the trimeric composition is envisioned by the inventor is a trimer consisting of three identical peptides.

The Rejections under 35 U.S.C. 112, second paragraph

Claims 19-22 have been rejected as allegedly indefinite. Applicants respectfully traverse this rejection.

The Patent Office has taken the position that these claims are indefinite because the term "a transition midpoint temperature" is not defined in the Specification, and because the claim is said to lack structural language.

Applicants respectfully note that Paragraph [0115] provides the following definition:

> $T_{1/2}$ is the transition midpoint temperature at which there is a 50% decrease in molar ellipticity $[\theta]_{222}$ compared to the fully folded peptide as determined by CD at 5 ^{o}C. All peptides in which $T_{1/2}$ was determined are boxed, for example, HR-N1, HR-N2, HR-N3, HR-N12, HR-C1, and HR-C4.

Accordingly, Applicants submit that the claims are clear to one of ordinary skill in the art in view of the clarifying definition provided in the Specification. It is believed that this definition of the transition midpoint temperature does not require that there is more than one peptide in association. In that the definition applies to a single peptide, it is believed that there is no "gap between the necessary structural connections", as alleged by the Patent Office.

In view of the foregoing, the withdrawal of this rejection is respectfully requested.

The Rejection under 35 U.S.C. 102

Claims 1-6, 8, 10, 19-23 and 37 have been rejected under 35 U.S.C. 102(e) as allegedly unpatentable over Rottier (US 2004-0071709, filed April 14, 2003). Applicants respectfully traverse this rejection.

The Patent Office has indicated that the cited Rottier reference teaches a 49 amino acid peptide derived from SARS CoV (Tort2), which peptide comprises a continuous sequence of 14 amino acids of SEQ ID NO:67 of the present claims. In the stretch of sequence provided, there is said that there is only one amino acid difference when amino acids 1-36 of instant SEQ ID NO:67 is compared with amino acids 7-42 of Rottier's SEQ ID NO:27. Rottier is said to teach that S proteins of SARS-CoV possess an α-helical trimeric conformation and that HR2 peptides of SARS can inhibit anti-parallel coiled coil formation of a coronavirus spike protein by decreasing contact between heptad repeat regions of the protein. They are further said to be potent antivirals.

In the interest of advancing prosecution and without acquiescing to the rejection, Applicants have amended claims 1, 6, 8, 9, 10, 19, to specify that the inhibitor peptide has a length from about 14 to about 35 amino acids (Inhibitor compounds are also generated comprising from about 14 residues to about 35 residues"). This is supported by the as-filed application in Paragraph [0172]. Applicants respectfully note that the peptide of Rottier consists of 49 amino acids. This is a different composition than the present claimed peptides specified to be from about 14 to about 35 amino acids in length.

In view of the foregoing discussion and the amendment to the claims, Applicants maintain the present claims are distinguished over the cited Rottier reference, and the rejection should be withdrawn.

The Rejection under 35 U.S.C. 103

The Patent Office has requested confirmation that the subject matter of the various claims was commonly owned at the time the invention was made.

It is confirmed that the subject matter of the various claims were commonly owned at the time the invention was made.

Claims 1-6, 8-11, 13, 19-23, 37 and 40-44 have been rejected under 35 U.S.C. 103(a) as allegedly unpatentable over Rottier (US 2004-0071709, filed April 14, 2003) in view of Kliger et al. (2003) BMC Microbiology 3:20. Applicants respectfully traverse this rejection.

Rottier was characterized above and is said to further teach HR2 sequence homology between DR2 of SARS-CoV and those of other coronaviruses. The Kliger reference is said to teach the C-terminal HR sequence, with reference to Fig. 3b, and Kliger is said to show the helical wheel of C-HR.

The Examiner has drawn on the KSR Supreme Court decision, alleging that it would have been obvious to one or ordinary skill in the art at the time the invention was made to make the HR-C4 analog of SEQ ID NO:67 by substituting Ile for Ala in order to make a more stable helix structure. The Examiner has further alleged that there would have been a reasonable probability of success in obtaining an analog, like that of SEQ ID NO:67.

Applicants respectfully submit that neither the cited Rottier reference (nor Kliger) teach or suggest that a peptide shorter than 47 amino acids would be useful in preventing SARS virus infection or that all peptides would be effective in blocking infection of cells. In Paragraph [0091] of the cited Rottier reference, it is stated that peptides HR1, HR1a, HR1b, HR1c and HR2 were tested for their abilities to inhibit virus entry into cells and of these, only HR2 "blocked viral entry in a concentration-dependent manner". However, the Examiner is correct that Fig. 10 shows a comparison of the

HR2 of several viruses and there is relatedness to SEQ ID NO:67. Thus, it is Applicants' position that the teachings of the cited reference do not clearly lead the skilled artisan to the particular region of the S protein modified to produce an inhibitor of virus infection, the inhibitor being a peptide of from about 14 to about 35 amino acids, with any reasonable probability of success.

Moreover, a direct comparison of present SEQ ID NO:67 with the MHV HR2 sequence shows, over the aligned length of 36 amino acids, there were only 12 identical residues. A comparison of SEQ ID NO:67 with the FIPv sequence reveals that there are only 8 residues identical in the aligned 36 amino acid sequence. Applicants do not see how this reference points the skilled artisan to the particular region of the protein or to a particular residue for change, i.e. the Ala to Ile substitution in the native SARS sequence at position 23. Given the large number of differences at a number of amino acid positions in the HR2 subregion related to SEQ ID NO:67, Applicants respect fully submit that position 23 is not called out as a particular amino acid of interest, given the overall differences in sequence.

As to the cited Kliger reference, Applicants believe it is best viewed as speculative: See the paragraph at fourth page, bottom right, where it is said "[p]eptides derived from the C-HR segment of SARS-CoV S2 protein... **might** inhibit viral induced membrane fusion, thereby blocking SARS-CoV infection" [emphasis added]. Comparing this sequence with the viral sequences in Fig. 10 of Rottier does not lead one to the particular Ala to Ile change embodied in SEQ ID NO:67. The cited Kliger reference does not supply what it is absent from the teachings of the Rottier reference.

In view of the foregoing, Applicants respectfully maintain that the present invention as claimed is not *prima facie* obvious over the cited references, and the rejection under 35 U.S.C. 103 should be withdrawn.

Conclusion

In view of the foregoing, it is submitted that this case is in condition for allowance, and passage to issuance is respectfully requested.

If there are any outstanding issues related to patentability, the courtesy of a telephone interview is requested, and the Examiner is invited to call to arrange a mutually convenient time.

This amendment is accompanied by a Petition for Extension of Time (three months) and payment in the amount of $555.00 as required under 37 C.F.R. 1.17(a). It is believed that this amendment does not necessitate the payment of any additional fees under 37 C.F.R. 1.16-1.17. If the amount submitted is incorrect, however, please charge the appropriate amount due under the foregoing Rules to Deposit Account No. 07-1969.

Respectfully submitted,

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